

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:51:21 ; Search time 35.44 Seconds

(without alignments)  
84.051 Million cell updates/sec

Title: US-09-785-059-3

Perfect score: 176

Sequence: 1 RMIRVQRCRAIRHMRIRGRLRWLV 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	50.6	861	1 VCLJLV	env polypeptide pr
2	88	50.0	856	1 VCLJ3W	env polypeptide pr
3	87	49.4	357	2 S21990	envelope protein g
4	87	49.4	358	2 S22002	envelope protein g
5	85	48.3	358	2 S22000	envelope protein g
6	85	48.3	358	2 S70417	envelope protein g
7	84	47.7	852	2 T12016	envelope glycoprote
8	82	46.6	846	1 VCLJND	env polypeptide pr
9	79	44.9	852	1 VCLJBR	env polypeptide pr
10	78	44.3	851	2 S33985	env polypeptide -
11	78	44.3	853	2 S54384	envelope polypeptide
12	78	44.3	856	1 VCLJH3	env polypeptide pr
13	78	44.3	856	1 VCLJH3	env polypeptide pr
14	77	43.8	855	1 VCLJVL	env polypeptide pr
15	76	43.2	357	2 S22006	envelope protein g
16	76	43.2	854	2 S13288	env polypeptide - huma
17	72	40.9	357	2 S21994	envelope protein g
18	70	39.8	868	1 VCLJH4	env polypeptide -
19	69	38.2	859	2 T01672	envelope polypeptide
20	68	38.6	357	2 S22004	envelope protein g
21	68	38.6	357	2 S21996	envelope protein g
22	68	38.6	357	2 S21992	envelope protein g
23	68	38.6	859	1 VCLJMN	env polypeptide pr
24	67	38.1	358	2 S21998	envelope protein g
25	67	38.1	861	1 VCLJSC	env polypeptide pr
26	66	37.5	847	2 T09448	env polypeptide pr
27	66	37.5	847	2 S13289	env polypeptide - huma
28	66	37.5	856	1 A44663	env polypeptide pr
29	65	36.9	843	1 H44001	env polypeptide pr

30	64	36.4	861	1 VCLJKB	env polypeptide pr
31	61.5	34.9	111	2 T14306	glycine-rich prote
32	60	34.1	855	1 VCLJZR	env polypeptide pr
33	59	33.5	396	2 I58168	growth factor arg3
34	58.5	33.2	1538	2 H70846	hypothetical glyci
35	58	33.0	854	1 VCLJST	env polypeptide pr
36	57	32.4	432	2 T05236	hypothetical prote
37	56	31.8	863	2 A53034	gag polypeptide -
38	54.5	31.0	998	1 Q08HB1	B1 protein A - black
39	54.5	31.0	998	2 S41397	protein A - black
40	54	30.7	173	2 S23732	MADS box protein P
41	53.5	30.4	153	2 F86331	F6P9.11 protein -
42	52.5	29.8	173	2 B83504	hypothetical prote
43	52	29.5	515	2 AH2996	glycerol-3-phospha
44	52	29.5	531	2 A98287	g1pd gene homolog
45	52	29.5	1459	2 T24088	hypothetical prote

#### ALIGNMENTS

RESULT 1  
VCLJLV  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; M0ID:85099333  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MA1>  
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Stc>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,337,344,361,391,397,402,  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status pre  
Query Match 50.6%; Score 89; DB 1; Length 861;  
Best Local Similarity 75.0%; Pred. No. 0.00063;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 RMIRVQRCRAIRHMRIRGRLRWLV 28  
DB 833 RVEIVQGCRAIRHMRIRGRLRWLV 860  
RESULT 2  
VCLJ3W  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the  
A:Reference number: A24774; M0ID:86218077  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:91906382  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: coat protein, glycoprotein, polypeptide, transmembrane protein  
F:1-2/Domain: signal sequence #status predicted <SIC>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 50.0%; Score 88; DB 1; Length 856;  
Best Local Similarity 75.0%; Pred. No. 0.00064;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 RWIRVQRCRAIRHTRIRGRLRML 28  
DB 828 RVIEVQRCRAIRHTRIRGRLRML 855

RESULT 3  
S21990  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 20  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
A:Accession: S21990; S70423  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A:Reference number: S21990  
A:Accession: S21990  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>  
A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; M0ID:92144209  
A:Accession: S70423  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-332, 'X', 334-357 <STE2>  
A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176  
C:Superfamily: type E retrovirus env polypeptide

Query Match 49.4%; Score 87; DB 2; Length 357;  
Best Local Similarity 71.4%; Pred. No. 0.00053;  
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RWIRVQRCRAIRHTRIRGRLRML 28  
DB 329 RVIEVQRCRAIRHTRIRGRLRML 356

RESULT 4  
S22002  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 3L  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
A:Accession: S22002; S70418  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A:Reference number: S21990  
A:Accession: S22002  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; M0ID:92144209

A:Accession: S70418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-333, 'X', 335-358 <STE2>  
A:Cross-references: EMBL:X61352; NID:g60186  
C:Superfamily: type E retrovirus env polypeptide

Query Match 49.4%; Score 87; DB 2; Length 358;  
Best Local Similarity 71.4%; Pred. No. 0.00053;  
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RWIRVQRCRAIRHTRIRGRLRML 28  
DB 330 RVIEVQRCRAIRHTRIRGRLRML 357

RESULT 5  
S22000  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
A:Accession: S22000  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A:Reference number: S21990  
A:Accession: S22000  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351  
C:Superfamily: type E retrovirus env polypeptide

Query Match 48.3%; Score 85; DB 2; Length 358;  
Best Local Similarity 71.4%; Pred. No. 0.00097;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RWIRVQRCRAIRHTRIRGRLRML 28  
DB 330 RVIEVQRCRAIRHTRIRGRLRML 357

RESULT 6  
S70417  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: patient 3B  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
A:Accession: S70417  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; M0ID:92144209  
A:Accession: S70417  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351; NID:g60184; PIDN:CAA43614.1; PID:g60185  
C:Superfamily: type E retrovirus env polypeptide

Query Match 48.3%; Score 85; DB 2; Length 358;  
Best Local Similarity 71.4%; Pred. No. 0.00097;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RWIRVQRCRAIRHTRIRGRLRML 28  
DB 330 RVIEVQRCRAIRHTRIRGRLRML 357

RESULT 7

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T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: 217379; MUID:9818716
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MC>
A:Cross-references: EMBL:U09034; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein

Query Match          47.7%; Score 84; DB 2; Length 852;
Best Local Similarity 71.4%; Pred. No. 0.0028;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  RWIRVQRMCRATRHITRRIRGGLRRML 28
DB      824  RVIEVQGRACRAITLHPRIROGLERL 851

RESULT  8
env polypotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polypotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00066
R:Spire, B.; Site, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immun
A:Reference number: J00065; MUID:90034200
A:Accession: J00066
A:Molecule type: DNA
A:Residues: 1-846 <SP>
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match          46.6%; Score 82; DB 1; Length 846;
Best Local Similarity 67.9%; Pred. No. 0.0051;
Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1  RWIRVQRMCRATRHITRRIRGGLRRML 28
DB      818  RVIEVQGRACRAITLHPRIROGLERL 845

RESULT  9
env polypotein - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polypotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1

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A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C:Accession: A31667
R:Rand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar
Virology 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (H
A:Reference number: A94389; MUID:89085613
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
C:Superfamily: type E retrovirus env polypotein
C:Keywords: capsid protein; coat protein; polypotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

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Query Match          44.9%; Score 79; DB 1; Length 852;
Best Local Similarity 69.0%; Pred. No. 0.013;
Matches 20; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1  RWIRVQRMCRATRHITRRIRGGLRRML 29
DB      824  RATEVQGRACRAITLHPRIROGLERLQ 852

RESULT 10
env polypotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlani, F.
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA7628.1; PID:g60199
C:Superfamily: type E retrovirus env polypotein

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Query Match          44.3%; Score 78; DB 2; Length 851;
Best Local Similarity 71.4%; Pred. No. 0.017;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  RWIRVQRMCRATRHITRRIRGGLRRML 28
DB      823  RVIEVQGRACRAITLHPRIROGLERL 850

RESULT 11
envelope polypotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
A:Title: The HIV-1 genome
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g3229377; PIDN:AAA5370.1; PID:g3229385
C:Superfamily: type E retrovirus env polypotein
C:Keywords: polypotein

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Query Match          44.3%; Score 78; DB 2; Length 853;
Best Local Similarity 60.7%; Pred. No. 0.017;
Matches 17; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

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